

In a preferred embodiment, a method provided by the invention uses as a target for *in situ* hybridisation a (16S) ribosomal RNA molecule. In a particular embodiment of the invention said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG (SEQ ID NO:1) or GTAGCCCTACTCGTAAGG (SEQ ID NO:2) or GAGCAAAGGTATTAAC TTTACTCCC (SEQ ID NO:3) or GTTAGCCGTCCCTTTCTGG (SEQ ID NO:4) or TTATCCCCCTCTGATGGG (SEQ ID NO:5) or AGAGAAGCAAGCTTCTCGTCCG (SEQ ID NO:6) or GCCACTCCTCTTTTCCGG (SEQ ID NO:7) or GCTAATGCAGCGCGGATCC (SEQ ID NO:8) or CCGAAGGGGAAGGCTCTA (SEQ ID NO:9) or AGAGAAGCAAGCTTCTCGTCCGTT (SEQ ID NO:10), each selected in relation to a method as provided by the invention or in relation to congruent antibiotic sensitivity of a bacterium recognised by said probe.

Please delete the last paragraph of page 9 and replace it with the following substitute paragraph.

—Such a positive or negative control probe as provided by the invention is given in the experimental part, in general said positive control probe comprises no more than five mismatches with a probe with the sequence GCTGCCTCCCGTAGGAGT (SEQ ID NO:11) and/or said negative control probe comprises no more than five mismatches with a probe with the sequence ACTCCTACGGGAGGCAGC (SEQ ID NO:12).

Please delete the second paragraph on page 10 and replace it with the following substitute paragraph.

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p In a preferred embodiment of the invention, such a probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG (SEQ ID NO:1) or GAGCAAAGGTATTAACCTTACTCCC (SEQ ID NO:3) (i.e. reactive with bacteria for which amoxycillin treatment is most likely effective) or GTAGCCCTACTCGTAAGG (SEQ ID NO:2) (cephalosporin treatment) or GTTAGCCGTCCCTTTCTGG (SEQ ID NO:4) (piperacillin and/or aminoglycoside) or TTATCCCCCTCTGATGGG (SEQ ID NO:5) or GCCACTCCTCTTTTCCGG (SEQ ID NO:7) (amoxycillin) or GCTAATGCAGCGCGGATCC (SEQ ID NO:8) or CCGAAGGGGAAGGCTCTA (SEQ ID NO:9) (vancomycin) or AGAGAAGCAAGCTTCTCGTCCGTT (SEQ ID NO:10) or AGAGAAGCAAGCTTCTCGTCCG (SEQ ID NO:6) (flucloxacilin).--

Please delete the table near the top of page 16 and insert in its place the following substitute table.

ID	Sequence (5'-3') ¹	Region ²	Specificity ³
A	GCTGCCTCCCGTAGGAGT (SEQ ID NO:11)	V2	Bacterial Kingdom
B	ACTCCTACGGGAGGCAG C (SEQ ID NO:12)	n.d.	no matches
C	GCCTGCCAGTTTCGAATG (SEQ ID NO:1)	V2	Saimoneilia spp., Kiebsiella spp., Enterobacter spp.
D	GTAGCCCTACTCGTAAG G (SEQ ID NO:2)	V7	K. oxytoca, S. marcescens, Enterobacter spp., Proteus spp.
E	GAGCAAAGGTATTA TTACTCCC (SEQ ID NO:3)	V3	E. coli
F	TTATCCCCCTCTGATGGG (SEQ ID NO:5)	V2	E. faecalis
G	GCTAATGCAGCGCGGAT CC (SEQ ID NO:8)	V2	S. aureus, S. haemolyticus
H	CCGAAGGGGAAGGCTCT A (SEQ ID NO:9)	V6	S. aureus, S. saprophyticus
I	AGAGAAGCAAGCTTCTC GTCCG (SEQ ID NO:6)	V1	Streptococcus spp.
J	GTTAGCCGTCCCTTTCTG G (SEQ ID NO:4)	V3	P. aeruginosa
K	AGAGAAGCAAGCTTCTC GTCCGTT (SEQ ID NO:10)	V2	S. aureus
L	GCCACTCCTCTTTTCCG G (SEQ ID NO:7)	??	Enterococcus faecium

Please delete Table 3 near the top of page 24 and substitute the following table in its place.

Probe*	Sequence (5'→3')	Target(s)	Preferred antibiotic**
EUB	GCTGCCTCCCGTAGG AGT (SEQ ID NO:11)	Bacterial Kingdom	n.a.***
non-EUB	ACTCCTACGGGAGGC AGC (SEQ ID NO:12)	negative control	n.a.
STREP	GTTAGCCGTCCTTT CTGG (SEQ ID NO:4)	<i>Streptococcus</i> spp.	Penicillin G
EFAEC	TTATCCCCCTCTGAT GGG (SEQ ID NO:5)	<i>Enterococcus faecalis</i>	Amoxycillin
EFAEM	GCCACTCCTCTTTT CCGG (SEQ ID NO:7)	<i>Enterococcus faecium</i>	Vancomycin
STAUR	AGAGAAGCAAGCTT CTCGTCCG (SEQ ID NO:6)	<i>Staphylococcus aureus</i>	Flucloxacillin
CNS	CGACGGCTAGCTCCA AATGGTTACT (SEQ ID NO:13)	Coagulase-negative Staphylococci	Vancomycin
ECOLI	GCAAAGGTATTA TTACTCCC (SEQ ID NO:14)	<i>Escherichia coli</i>	Amoxycillin
PSEUDA ER	GGACGTTATCCCCA CTAT (SEQ ID NO:15)	<i>Pseudomonas aeruginosa</i>	Piperacillin+ aminoglycoside
ENTBAC	CATGAATCACAAAGT GGTAAGCGCC (SEQ ID NO:16)	<i>Enterobacterium</i> spp.	2 nd generation cephalosporin

IN THE CLAIMS

Please amend the following claims to read as follows.

more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG (SEQ ID NO:1) or